CLAIMS

1. Nucleotides encoding the full length or part of the nucleocapsid (NP) protein of Newcastle disease virus (NDV).

2. The nucleotides as claimed in claim 1 characterised in that it has the following nucleotide sequence:

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        10          20          30          40          50          60
ATGTCTTCCG TATTCGATGA ATACGAGCAG CTCCTCGCTG CTCAGACTCG CCCCAATGGA

        70          80          90         100         110         120
GCTCACGGAG GGGGAGAGAG AGGGAGCACT TTAAGAGTTG AGGTCCCAGT ATTCACTCTT

       130         140         150         160         170         180
AACAGTGACG ATCCAGAAGA TAGATGGAAT TTTGCGGTAT TCTGTCTTCG GATTGCTGTT

       190         200         210         220         230         240
AGCGAGGACG CCAACAAACC GCTCAGGCAA GGTGCTCTCA TATCCCTCCT GTGCTCCCAT

       250         260         270         280         290         300
TCTCAAGTGA TGAGGAACCA TGTTGCCCTT GCAGGAAAAC AGAATGAGGC TACACTGACT

       310         320         330         340         350         360
GTTCTTGAGA TCGATGGTTT TACCAGCAGC GTGCCTCAGT TCAACAACAG GAGTGGGGTG

       370         380         390         400         410         420
TCTGAGGAGA GAGCACAGAG ATTCATGGTG ATAGCAGGGT CTCTCCCTCG GGCGTGCAGT

       430         440         450         460         470         480
AACGGTACTC CGTTCGTCAC GGCTGGGGTT GAAGATGATG CACCAGAAGA TATCACTGAT

       490         500         510         520         530         540
ACTCTGGAAA GAATCCTGTC TATCCAGGCT CAGGTATGGG TCACAGTAGC GAAGGCCATG

       550         560         570         580         590         600
ACTGCATATG AGACAGCAGA TGAGTCGGAA ACAAGAAGAA TCAATAAGTA CATGCAGCAA

       610         620         630         640         650         660
GGCAGAGTCC AGAAGAAGTA CATCCTCCAC CCTGTATGCA GGAGTGCAAT TCAACTCACA

       670         680         690         700         710         720
ATCAGACATT CTCTGGCAGT CCGCATTTTC TTAGTTAGCG AGCTTAAGAG AGGCCGCAAT

       730         740         750         760         770         780
ACGGCAGGTG GGAGCTCCAC GTATTACAAC TTAGTAGGGG ATGTAGACTC ATACATCAGG

       790         800         810         820         830         840
AACACCGGAC TTACTGCATT CTTCCTTACA CTCAAATATG GAATTAATAC CAAGACATCA
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          850         860         870         880         890         900
GCCCTAGCAC TCAGCAGCCT CACAGGCGAT ATCCAAAAGA TGAAGCAGCT CATGCGTTTA

          910         920         930         940         950         960
TATCGGATGA AGGGAGAAAA TGCGCCGTAC ATGACATTGC TAGGTGACAG TGATCAGATG

          970         980         990        1000        1010        1020
AGCTTTGCAC CGGCTGAGTA TGCACAGCTT TATTCTTTTG CCATGGGCAT GGCATCAGTC

         1030        1040        1050        1060        1070        1080
TTAGATAAAG GAACTGGCAA ATACCAATTC GCCAGAGACT TCATGAGCAC ATCATTCTGG

         1090        1100        1110        1120        1130        1140
AGACTCGGGG TGGAGTATGC TCAGGCTCAG GGGAGTAGCA TCAACGAAGA CATGGCTGCT

         1150        1160        1170        1180        1190        1200
GAGCTAAAAC TAACCCCGGC AGCAAGAAGG GGCCTGGCAG CTGCTGCCCA ACGAGTGTCT

         1210        1220        1230        1240        1250        1260
GAGGAAACTG GCAGCGTGGA TATTCCTACT CAACAAGCCG GGGTCCTCAC TGGGCTCAGC

         1270        1280        1290        1300        1310        1320
GATGGAGGCC CCCGAGCCTC TCAGGGTGGA TCGAACAAGT CGCAAGGGCA ACCAGATGCC

         1330        1340        1350        1360        1370        1380
GGAGATGGGG AGACCCAATT CTTGGATTTG ATGAGAGCAG TGGCGAACAG CATGCGAGAA

         1390        1400        1410        1420        1430        1440
GCGCCAAACT CCGCACAGAG CACCACCCAC CCGGAACCCC CCCCGACTCC CGGGCCATCA

         1450        1460        1470        1480        1490        1500
CAAGATAACG ACACCGACTG GGGGTATTGA ..........  ..........  ..........
```

3. Nucleotides encoding the full length or part of the phosphoprotein (P) of Newcastle disease virus (NDV).

4. The nucleotides as claimed in claim 3 characterised in that it has the following nucleotide sequence:

```
           10          20          30          40          50          60
ATGGCCACCT TTACAGATGC GGAGATAGAT GATATATTTG AGACCAGTGG AACTGTCATT

           70          80          90         100         110         120
GACAGCATAA TTACGGCCCA GGGTAAATCA GCAGAGACTG TCGGAAGGAG CGCAATCCCA

          130         140         150         160         170         180
CAAGGCAAGA CCAAAGCGCT GAGCATAGCA TGGGAGAAGC ATGGGAGCAT CCAACCATCC

          190         200         210         220         230         240
ACCAGCCAGG ACAACCCCGA CCAACAGGAT AGACCAGACA AACAGCTATC CACACCTGAG

          250         260         270         280         290         300
CAGGCGACCC CACACAACAG CTCGCCAGCC ACATCCGCCG AACCGCTCCC CACTCAGGCC
```

```
          310         320         330         340         350         360
GCAGGTGAGG CCGGCGACAC ACAGCTCAAG ACCGGAGCAA GCAACTCTCT TCTGTCTATG

          370         380         390         400         410         420
CTCGACAAGC TGAGCAATAA ACCATCTAAT GCTAAAAAGG GCCCATGGTC GAGTCCCCAG

          430         440         450         460         470         480
GAAGGATATC ATCAACCTCC GACCCAACAA CATGGGGATC AGCCGAACCG CGGAAACAGC

          490         500         510         520         530         540
CAGGAGAGGC TGCGGCACCA AGCCAAGGCC GCCCCTGGAA GCCGGGGCAC AGACGCGAGC

          550         560         570         580         590         600
ACAGCATATC ATGGACAATG GAAGGAGTCA CAACTATCAG CTGGTGCAAC CCCTCATGTG

          610         620         630         640         650         660
CTCCAATCAG GGCAGAGCCA AGACAGTACT CCTGTACCTG TGGATCATGT CCAGCCACCT

          670         680         690         700         710         720
GTCGACTTTG TGCAGGCGAT GATGACTATG ATGGAGGCGT TATCACAGAA GGTAAGTAAA

          730         740         750         760         770         780
GTCGACTATC AGCTAGACCT AGTCTTAAAG CAGACATCCT CCATCCCTAT GATGCGGTCT

          790         800         810         820         830         840
GAAATCCAAC AGCTAAAAAC ATCTGTTGCG GTCATGGAAG CTAATTTAGG CATGATGAAA

          850         860         870         880         890         900
ATTCTGGACC CTGGTTGTGC TAACATTTCA TCCTTAAGTG ATCTGCGGGC AGTCGCCCGG

          910         920         930         940         950         960
TCCCACCCAG TTTTAATTTC AGGCCCCGGA GATCCGTCCC CCTACGTGAC ACAAGGGGGT

          970         980         990        1000        1010        1020
GAGATGACAC TCAATAAACT CTCACAACCA GTACAACACC CTTCCGAGTT AATTAAATCT

         1030        1040        1050        1060        1070        1080
GCCACAGCGG GCGGACCTGA TATGGGAGTG GAAAAGGACA CTGTCCGTGC ATTGATCACC

         1090        1100        1110        1120        1130        1140
TCGCGCCCGA TGCATCCAAG CTCCTCAGCT AAGCTCCTGA GTAAGCTGGA TGCAGCCGGG

         1150        1160        1170        1180        1190        1200
TCGATTGAAG AGATCAGAAA GATCAAGCGC CTTGCACTAA ATGGCTAA.. ..........
```

5. The NP protein coded according to claim 1 or claim 2 characterised in that it has the following amino acid sequence:

```
  1  M   S   S   V   F   D   E   Y   E   Q   L   L   A   A   Q   T        16
     ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
     1           10          20          30          40

 17  R   P   N   G   A   H   G   G   G   E   R   G   S   T   L   R        32
     CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
     50          60          70          80          90
```

```
33   V  E  V  P  V  F  T  L  N  S  D  D  P  E  D  R   48
     GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA
      100        110        120        130        140

49   W  N  F  A  V  F  C  L  R  I  A  V  S  E  D  A   64
     TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC
      150        160        170        180        190

65   N  K  P  L  R  Q  G  A  L  I  S  L  L  C  S  H   80
     AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT
      200        210        220        230        240

81   S  Q  V  M  R  N  H  V  A  L  A  G  K  Q  N  E   96
     TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG
      250        260        270        280

97   A  T  L  T  V  L  E  I  D  G  F  T  S  S  V  P  112
     GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT
290        300        310        320        330

113  Q  F  N  N  R  S  G  V  S  E  E  R  A  Q  R  F  128
     CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC
      340        350        360        370        380

129  M  V  I  A  G  S  L  P  R  A  C  S  N  G  T  P  144
     ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG
      390        400        410        420        430

145  F  V  T  A  G  V  E  D  D  A  P  E  D  I  T  D  160
     TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT
      440        450        460        470        480

161  T  L  E  R  I  L  S  I  Q  A  Q  V  W  V  T  V  176
     ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA
      490        500        510        520

177  A  K  A  M  T  A  Y  E  T  A  D  E  S  E  T  R  192
     GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA
530        540        550        560        570

193  R  I  N  K  Y  M  Q  Q  G  R  V  Q  K  K  Y  I  208
     AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC
      580        590        600        610        620

209  L  H  P  V  C  R  S  A  I  Q  L  T  I  R  H  S  224
     CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT
      630        640        650        660        670

225  L  A  V  R  I  F  L  V  S  E  L  K  R  G  R  N  240
     CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT
      680        690        700        710        720

241  T  A  G  G  S  S  T  Y  Y  N  L  V  G  D  V  D  256
     ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC
      730        740        750        760

257  S  Y  I  R  N  T  G  L  T  A  F  F  L  T  L  K  272
     TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA
770        780        790        800        810

273  Y  G  I  N  T  K  T  S  A  L  A  L  S  S  L  T  288
     TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA
      820        830        840        850        860

289  G  D  I  Q  K  M  K  Q  L  M  R  L  Y  R  M  K  304
     GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG
      870        880        890        900        910
```

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305  G   E   N   A   P   Y   M   T   L   L   G   D   S   D   Q   M   320
     GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG
               920         930         940         950         960

321  S   F   A   P   A   E   Y   A   Q   L   Y   S   F   A   M   G   336
     AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC
           970         980         990        1000

337  M   A   S   V   L   D   K   G   T   G   K   Y   Q   F   A   R   352
     ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA
1010        1020        1030        1040        1050

353  D   F   M   S   T   S   F   W   R   L   G   V   E   Y   A   Q   368
     GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG
1060        1070        1080        1090        1100

369  A   Q   G   S   S   I   N   E   D   M   A   A   E   L   K   L   384
     GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA
1110        1120        1130        1140        1150

385  T   P   A   A   R   R   G   L   A   A   A   A   Q   R   V   S   400
     ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT
1160        1170        1180        1190        1200

401  E   E   T   G   S   V   D   I   P   T   Q   Q   A   G   V   L   416
     GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC
1210        1220        1230        1240

417  T   G   L   S   D   G   G   P   R   A   S   Q   G   G   S   N   432
     ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC
1250        1260        1270        1280        1290

433  K   S   Q   G   Q   P   D   A   G   D   G   E   T   Q   F   L   448
     AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG
1300        1310        1320        1330        1340

449  D   L   M   R   A   V   A   N   S   M   R   E   A   P   N   S   464
     GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
1350        1360        1370        1380        1390

465  A   Q   S   T   T   H   P   E   P   P   P   T   P   G   P   S   480
     GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
1400        1410        1420        1430        1440

481  Q   D   N   D   T   D   W   G   Y   *                           490
     CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
1450        1460        1470
```

6. The P protein coded according to claim 3 or claim 4 characterised in that it has the following amino acid sequence:

```
 1   M   A   T   F   T   D   A   E   I   D   D   I   F   E   T   S   16
     ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
     1           10          20          30          40

17   G   T   V   I   D   S   I   I   T   A   Q   G   K   S   A   E   32
     GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
     50          60          70          80          90
```

```
33  T  V  G  R  S  A  I  P  Q  G  K  T  K  A  L  S                    48
    ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC
    100         110         120         130         140

49  I  A  W  E  K  H  G  S  I  Q  P  S  T  S  Q  D                    64
    ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
    150         160         170         180         190

65  N  P  D  Q  Q  D  R  P  D  K  Q  L  S  T  P  E                    80
    AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG
    200         210         220         230         240

81  Q  A  T  P  H  N  S  S  P  A  T  S  A  E  P  L                    96
    CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
    250         260         270         280

97  P  T  Q  A  A  G  E  A  G  D  T  Q  L  K  T  G                   112
    CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
290         300         310         320         330

113 A  S  N  S  L  L  S  M  L  D  K  L  S  N  K  P                   128
    GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
    340         350         360         370         380

129 S  N  A  K  K  G  P  W  S  S  P  Q  E  G  Y  H                   144
    TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
    390         400         410         420         430

145 Q  P  P  T  Q  Q  H  G  D  Q  P  N  R  G  N  S                   160
    CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC
    440         450         460         470         480

161 Q  E  R  L  R  H  Q  A  K  A  A  P  G  S  R  G                   176
    CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC
    490         500         510         520

177 T  D  A  S  T  A  Y  H  G  Q  W  K  E  S  Q  L                   192
    ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA
530         540         550         560         570

193 S  A  G  A  T  P  H  V  L  Q  S  G  Q  S  Q  D                   208
    TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC
    580         590         600         610         620

209 S  T  P  V  P  V  D  H  V  Q  P  P  V  D  F  V                   224
    AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG
    630         640         650         660         670

225 Q  A  M  M  T  M  M  E  A  L  S  Q  K  V  S  K                   240
    CAG GCG ATG ATG ACT ATG ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA
    680         690         700         710         720

241 V  D  Y  Q  L  D  L  V  L  K  Q  T  S  S  I  P                   256
    GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT
    730         740         750         760

257 M  M  R  S  E  I  Q  Q  L  K  T  S  V  A  V  M                   272
    ATG ATG CGG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG
770         780         790         800         810

273 E  A  N  L  G  M  M  K  I  L  D  P  G  C  A  N                   288
    GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC
    820         830         840         850         860

289 I  S  S  L  S  D  L  R  A  V  A  R  S  H  P  V                   304
    ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC CGG TCC CAC CCA GTT
    870         880         890         900         910
```

```
305   L   I   S   G   P   G   D   P   S   P   Y   V   T   Q   G   G      320
      TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
                920         930         940         950         960

321   E   M   T   L   N   K   L   S   Q   P   V   Q   H   P   S   E      336
      GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
              970         980         990        1000

337   L   I   K   S   A   T   A   G   G   P   D   M   G   V   E   K      352
      TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
    1010        1020        1030        1040        1050

353   D   T   V   R   A   L   I   T   S   R   P   M   H   P   S   S      368
      GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
     1060        1070        1080        1090        1100

369   S   A   K   L   L   S   K   L   D   A   A   G   S   I   E   E      384
      TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
        1110        1120        1130        1140        1150

385   I   R   K   I   K   R   L   A   L   N   G   *                      396
      ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
            1160        1170        1180
```

7. A recombinant expression plasmid containing the NDV nucleocapsid gene as claimed in claim 1 or claim 2.

8. A recombinant expression plasmid containing the NDV phosphoprotein gene as claimed in claim 3 or claim 4.

9. The recombinant expression plasmid according to claim 7 which is the expression plasmid pTrcHis2-NP constructed by cloning the NDV nucleocapsid gene of claims 1 or 2 into vector pTrcHis2.

10. The recombinant expression plasmid according to claim 8 which is the expression plasmid pTrcHis2-P constructed by cloning the NDV phosphoprotein gene of claims 3 or 4 into vector pTrcHis2.

11. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 7 or claim 9.

12. A transformed *Escherichia coli* with the recombinant expression plasmid according to claim 8 or claim 10.

13. The transformed microorganism according to claim 11, which is the transformed *E. coli* TOP10 (pTrcHis2-NP) produced by introducing the recombinant expression plasmid of claim 7 or claim 9 into *E. coli* TOP10.

14. The transformed microorganism according to claim 12, which is the transformed *E. coli* (pTrcHis2-P) produced by introducing the recombinant expression plasmid of claim 8 or claim 10 into *E. coli* TOP 10.

15. A fused or non-fused form of NDV nucleocapsid protein isolated and purified from culture of the transformed microorganism of claim 11 or claim 13 characterised in that it has the following amino acid sequence:


```
  1  M  S  S  V  F  D  E  Y  E  Q  L  L  A  A  Q  T   16
ATG TCT TCC GTA TTC GAT GAA TAC GAG CAG CTC CTC GCT GCT CAG ACT
  1          10         20         30         40

 17  R  P  N  G  A  H  G  G  G  E  R  G  S  T  L  R   32
CGC CCC AAT GGA GCT CAC GGA GGG GGA GAG AGA GGG AGC ACT TTA AGA
 50         60         70         80         90

 33  V  E  V  P  V  F  T  L  N  S  D  D  P  E  D  R   48
GTT GAG GTC CCA GTA TTC ACT CTT AAC AGT GAC GAT CCA GAA GAT AGA
100        110        120        130        140

 49  W  N  F  A  V  F  C  L  R  I  A  V  S  E  D  A   64
TGG AAT TTT GCG GTA TTC TGT CTT CGG ATT GCT GTT AGC GAG GAC GCC
150        160        170        180        190

 65  N  K  P  L  R  Q  G  A  L  I  S  L  L  C  S  H   80
AAC AAA CCG CTC AGG CAA GGT GCT CTC ATA TCC CTC CTG TGC TCC CAT
200        210        220        230        240

 81  S  Q  V  M  R  N  H  V  A  L  A  G  K  Q  N  E   96
TCT CAA GTG ATG AGG AAC CAT GTT GCC CTT GCA GGA AAA CAG AAT GAG
250        260        270        280

 97  A  T  L  T  V  L  E  I  D  G  F  T  S  S  V  P  112
GCT ACA CTG ACT GTT CTT GAG ATC GAT GGT TTT ACC AGC AGC GTG CCT
290        300        310        320        330

113  Q  F  N  N  R  S  G  V  S  E  E  R  A  Q  R  F  128
CAG TTC AAC AAC AGG AGT GGG GTG TCT GAG GAG AGA GCA CAG AGA TTC
340        350        360        370        380

129  M  V  I  A  G  S  L  P  R  A  C  S  N  G  T  P  144
ATG GTG ATA GCA GGG TCT CTC CCT CGG GCG TGC AGT AAC GGT ACT CCG
390        400        410        420        430

145  F  V  T  A  G  V  E  D  D  A  P  E  D  I  T  D  160
TTC GTC ACG GCT GGG GTT GAA GAT GAT GCA CCA GAA GAT ATC ACT GAT
440        450        460        470        480

161  T  L  E  R  I  L  S  I  Q  A  Q  V  W  V  T  V  176
ACT CTG GAA AGA ATC CTG TCT ATC CAG GCT CAG GTA TGG GTC ACA GTA
490        500        510        520
```

```
177   A   K   A   M   T   A   Y   E   T   A   D   E   S   E   T   R     192
      GCG AAG GCC ATG ACT GCA TAT GAG ACA GCA GAT GAG TCG GAA ACA AGA
    530         540         550         560         570

193   R   I   N   K   Y   M   Q   Q   G   R   V   Q   K   K   Y   I     208
      AGA ATC AAT AAG TAC ATG CAG CAA GGC AGA GTC CAG AAG AAG TAC ATC
      580         590         600         610         620

209   L   H   P   V   C   R   S   A   I   Q   L   T   I   R   H   S     224
      CTC CAC CCT GTA TGC AGG AGT GCA ATT CAA CTC ACA ATC AGA CAT TCT
      630         640         650         660         670

225   L   A   V   R   I   F   L   V   S   E   L   K   R   G   R   N     240
      CTG GCA GTC CGC ATT TTC TTA GTT AGC GAG CTT AAG AGA GGC CGC AAT
          680         690         700         710         720

241   T   A   G   G   S   S   T   Y   Y   N   L   V   G   D   V   D     256
      ACG GCA GGT GGG AGC TCC ACG TAT TAC AAC TTA GTA GGG GAT GTA GAC
              730         740         750         760

257   S   Y   I   R   N   T   G   L   T   A   F   F   L   T   L   K     272
      TCA TAC ATC AGG AAC ACC GGA CTT ACT GCA TTC TTC CTT ACA CTC AAA
    770         780         790         800         810

273   Y   G   I   N   T   K   T   S   A   L   A   L   S   S   L   T     288
      TAT GGA ATT AAT ACC AAG ACA TCA GCC CTA GCA CTC AGC AGC CTC ACA
      820         830         840         850         860

289   G   D   I   Q   K   M   K   Q   L   M   R   L   Y   R   M   K     304
      GGC GAT ATC CAA AAG ATG AAG CAG CTC ATG CGT TTA TAT CGG ATG AAG
          870         880         890         900         910

305   G   E   N   A   P   Y   M   T   L   L   G   D   S   D   Q   M     320
      GGA GAA AAT GCG CCG TAC ATG ACA TTG CTA GGT GAC AGT GAT CAG ATG
              920         930         940         950         960

321   S   F   A   P   A   E   Y   A   Q   L   Y   S   F   A   M   G     336
      AGC TTT GCA CCG GCT GAG TAT GCA CAG CTT TAT TCT TTT GCC ATG GGC
          970         980         990        1000

337   M   A   S   V   L   D   K   G   T   G   K   Y   Q   F   A   R     352
      ATG GCA TCA GTC TTA GAT AAA GGA ACT GGC AAA TAC CAA TTC GCC AGA
    1010        1020        1030        1040        1050

353   D   F   M   S   T   S   F   W   R   L   G   V   E   Y   A   Q     368
      GAC TTC ATG AGC ACA TCA TTC TGG AGA CTC GGG GTG GAG TAT GCT CAG
      1060        1070        1080        1090        1100

369   A   Q   G   S   S   I   N   E   D   M   A   A   E   L   K   L     384
      GCT CAG GGG AGT AGC ATC AAC GAA GAC ATG GCT GCT GAG CTA AAA CTA
        1110        1120        1130        1140        1150

385   T   P   A   A   R   R   G   L   A   A   A   A   Q   R   V   S     400
      ACC CCG GCA GCA AGA AGG GGC CTG GCA GCT GCT GCC CAA CGA GTG TCT
          1160        1170        1180        1190        1200

401   E   E   T   G   S   V   D   I   P   T   Q   Q   A   G   V   L     416
      GAG GAA ACT GGC AGC GTG GAT ATT CCT ACT CAA CAA GCC GGG GTC CTC
              1210        1220        1230        1240

417   T   G   L   S   D   G   G   P   R   A   S   Q   G   G   S   N     432
      ACT GGG CTC AGC GAT GGA GGC CCC CGA GCC TCT CAG GGT GGA TCG AAC
    1250        1260        1270        1280        1290

433   K   S   Q   G   Q   P   D   A   G   D   G   E   T   Q   F   L     448
      AAG TCG CAA GGG CAA CCA GAT GCC GGA GAT GGG GAG ACC CAA TTC TTG
        1300        1310        1320        1330        1340
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449  D   L   M   R   A   V   A   N   S   M   R   E   A   P   N   S   464
     GAT TTG ATG AGA GCA GTG GCG AAC AGC ATG CGA GAA GCG CCA AAC TCC
          1350            1360            1370            1380
465  A   Q   S   T   T   H   P   E   P   P   P   T   P   G   P   S   480
     GCA CAG AGC ACC ACC CAC CCG GAA CCC CCC CCG ACT CCC GGG CCA TCC
          1400            1410            1420            1430
481  Q   D   N   D   T   D   W   G   Y   *                           490
     CAA GAT AAC GAC ACC GAC TGG GGG TAT TGA
          1450            1460            1470
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16. A fused or non-fused form of NDV phosphoprotein isolated and purified from culture of the transformed microorganism of claim 12 or claim 14 characterised in that it has the following amino acid sequence:

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1    M   A   T   F   T   D   A   E   I   D   D   I   F   E   T   S   16
     ATG GCC ACC TTT ACA GAT GCG GAG ATA GAT GAT ATA TTT GAG ACC AGT
     1           10              20              30              40
17   G   T   V   I   D   S   I   I   T   A   Q   G   K   S   A   E   32
     GGA ACT GTC ATT GAC AGC ATA ATT ACG GCC CAG GGT AAA TCA GCA GAG
     50              60              70              80              90
33   T   V   G   R   S   A   I   P   Q   G   K   T   K   A   L   S   48
     ACT GTC GGA AGG AGC GCA ATC CCA CAA GGC AAG ACC AAA GCG CTG AGC
     100             110             120             130             140
49   I   A   W   E   K   H   G   S   I   Q   P   S   T   S   Q   D   64
     ATA GCA TGG GAG AAG CAT GGG AGC ATC CAA CCA TCC ACC AGC CAG GAC
          150             160             170             180             190
65   N   P   D   Q   Q   D   R   P   D   K   Q   L   S   T   P   E   80
     AAC CCC GAC CAA CAG GAT AGA CCA GAC AAA CAG CTA TCC ACA CCT GAG
               200             210             220             230             240
81   Q   A   T   P   H   N   S   S   P   A   T   S   A   E   P   L   96
     CAG GCG ACC CCA CAC AAC AGC TCG CCA GCC ACA TCC GCC GAA CCG CTC
               250             260             270             280
97   P   T   Q   A   A   G   E   A   G   D   T   Q   L   K   T   G   112
     CCC ACT CAG GCC GCA GGT GAG GCC GGC GAC ACA CAG CTC AAG ACC GGA
290             300             310             320             330
113  A   S   N   S   L   L   S   M   L   D   K   L   S   N   K   P   128
     GCA AGC AAC TCT CTT CTG TCT ATG CTC GAC AAG CTG AGC AAT AAA CCA
     340             350             360             370             380
129  S   N   A   K   K   G   P   W   S   S   P   Q   E   G   Y   H   144
     TCT AAT GCT AAA AAG GGC CCA TGG TCG AGT CCC CAG GAA GGA TAT CAT
          390             400             410             420             430
145  Q   P   P   T   Q   Q   H   G   D   Q   P   N   R   G   N   S   160
     CAA CCT CCG ACC CAA CAA CAT GGG GAT CAG CCG AAC CGC GGA AAC AGC
               440             450             460             470             480
161  Q   E   R   L   R   H   Q   A   K   A   A   P   G   S   R   G   176
     CAG GAG AGG CTG CGG CAC CAA GCC AAG GCC GCC CCT GGA AGC CGG GGC
               490             500             510             520
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177   T   D   A   S   T   A   Y   H   G   Q   W   K   E   S   Q   L   192
      ACA GAC GCG AGC ACA GCA TAT CAT GGA CAA TGG AAG GAG TCA CAA CTA
    530             540             550             560             570

193   S   A   G   A   T   P   H   V   L   Q   S   G   Q   S   Q   D   208
      TCA GCT GGT GCA ACC CCT CAT GTG CTC CAA TCA GGG CAG AGC CAA GAC
      580             590             600             610             620

209   S   T   P   V   P   V   D   H   V   Q   P   P   V   D   F   V   224
      AGT ACT CCT GTA CCT GTG GAT CAT GTC CAG CCA CCT GTC GAC TTT GTG
          630             640             650             660             670

225   Q   A   M   M   T   M   M   E   A   L   S   Q   K   V   S   K   240
      CAG GCG ATG ATG ACT ATG ATG GAG GCG TTA TCA CAG AAG GTA AGT AAA
              680             690             700             710             720

241   V   D   Y   Q   L   D   L   V   L   K   Q   T   S   S   I   P   256
      GTC GAC TAT CAG CTA GAC CTA GTC TTA AAG CAG ACA TCC TCC ATC CCT
              730             740             750             760

257   M   M   R   S   E   I   Q   Q   L   K   T   S   V   A   V   M   272
      ATG ATG CGG TCT GAA ATC CAA CAG CTA AAA ACA TCT GTT GCG GTC ATG
    770             780             790             800             810

273   E   A   N   L   G   M   M   K   I   L   D   P   G   C   A   N   288
      GAA GCT AAT TTA GGC ATG ATG AAA ATT CTG GAC CCT GGT TGT GCT AAC
      820             830             840             850             860

289   I   S   S   L   S   D   L   R   A   V   A   R   S   H   P   V   304
      ATT TCA TCC TTA AGT GAT CTG CGG GCA GTC GCC CGG TCC CAC CCA GTT
          870             880             890             900             910

305   L   I   S   G   P   G   D   P   S   P   Y   V   T   Q   G   G   320
      TTA ATT TCA GGC CCC GGA GAT CCG TCC CCC TAC GTG ACA CAA GGG GGT
              920             930             940             950             960

321   E   M   T   L   N   K   L   S   Q   P   V   Q   H   P   S   E   336
      GAG ATG ACA CTC AAT AAA CTC TCA CAA CCA GTA CAA CAC CCT TCC GAG
          970             980             990             1000

337   L   I   K   S   A   T   A   G   G   P   D   M   G   V   E   K   352
      TTA ATT AAA TCT GCC ACA GCG GGC GGA CCT GAT ATG GGA GTG GAA AAG
    1010            1020            1030            1040            1050

353   D   T   V   R   A   L   I   T   S   R   P   M   H   P   S   S   368
      GAC ACT GTC CGT GCA TTG ATC ACC TCG CGC CCG ATG CAT CCA AGC TCC
      1060            1070            1080            1090            1100

369   S   A   K   L   L   S   K   L   D   A   A   G   S   I   E   E   384
      TCA GCT AAG CTC CTG AGT AAG CTG GAT GCA GCC GGG TCG ATT GAA GAG
          1110            1120            1130            1140            1150

385   I   R   K   I   K   R   L   A   L   N   G   *                   396
      ATC AGA AAG ATC AAG CGC CTT GCA CTA AAT GGC TAA
              1160            1170            1180
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